

Probe Set Name	Gene Symbol	Gene Title	Average/S2 (YFP-LE)/L.monocyctogenes (wt)/8h after addition	1.3048	1.2525	1.43614	1.925	1.48183	0.025	1.25	2.75	0.44347	3.375	0.05	1.075	0.45735	1.05	0.05774
1626910_at	CG15282	CG15282	3.025	0.05	2.3	0.11547	2.175	1.02103	1.875	1.01448	2.7	0.18257	3.225	0.09574	1.775	0.12583	0.975	0.09574
1632964_at	CG15678	CG15678	3.475	1.68201	1.025	1.91551	0.975	2.19298	-0.425	2.03204	1.6	0.1633	3.1	0.29439	0.825	0.29854	1.35	0.23805
1633812_at	CG9080	CG9080	2.8	0.23094	1.65	0.23805	-2.875	2.05649	0.125	0.20616	2.3	0.2582	2.6	0.46904	1.525	0.22174	1.275	0.44253
1639469_a_at	Pa	GTP cyclohydrolase	3.45	0.56862	0.475	0.25	1.35	0.91104	0.25	0.1291	2.525	0.29861	1.975	0.3304	1.35	0.09075	0.775	0.32016
1623016_at	CG1299	CG1299	2.3	0.50662	1	1.33417	-0.05	1.65429	-0.325	1.14127	0.75	0.17321	1.85	0.23805	0.35	0.19149	0.4	0.18257
1623248_at	CG9452	CG9452	2.9	0.21602	1.625	1.1644	0.975	0.95	1.1	1.42595	-0.375	1.80808	1.7	1.76446	-0.375	1.37447	2.05	0.87369
1623385_at	---	---	2.35	0.41633	2.225	0.99791	-0.575	1.29711	1.125	1.22577	0.925	0.22174	1.6	0.08165	1.025	0.27538	1.075	0.17078
1630163_at	CG32373	CG32373	2.9	0.08165	1.975	0.38622	1.2	0.52281	0.225	0.49781	0.8	0.1633	1.225	0.20616	0.425	0.20616	-0.05	0.23805
1627073_a_at	CG10126	CG10126	2.825	0.80571	0.225	0.83815	1.55	1.06615	0.55	1.45258	-0.05	1.30256	1.15	0.17321	0.275	1.5756	1.875	0.57373
1628949_at	shn	quo vadis	2.525	0.64885	0.75	0.9037	0.6	1.57692	0.4	1.65328	0.325	0.15	0.975	0.61847	0.55	0.25166	1.5	0.52281
1632539_at	GstE4	Glutathione S transferase E4	2.5	1.80185	0.15	0.77244	1.05	0.52599	1.25	0.98826	-1.175	1.5756	0.9	0.42426	-0.025	1.04043	0.375	0.1893
1624452_a_at	ple	tyrosine hydroxylase	2.725	0.05	2.15	0.17321	-0.5	0.70711	0.9	0.7208	0.975	0.4272	0.825	0.17078	0.55	0.31091	0.3	0.14142
1636293_at	CG2217	CG2217	2.425	0.44253	1.225	1.09049	-1.3	2.74155	0.175	0.77449	0.5	0.1633	0.725	0.32016	0.125	0.12583	0.025	0.263
1640201_at	retnophilin	retnophilin	2.5	0.41633	6.9E-18	0.21602	-1.075	1.70171	-1.025	1.15866	0.325	0.20616	0.725	0.32016	0.2	0.11547	-0.025	0.25
1640614_at	cac	nightblind	2.425	0.49917	-0.075	0.17078	1.5	1.39523	1.425	1.56498	-0.2	1.84029	0.7	1.14891	-0.425	1.73853	0.9	1.32916
1634513_at	---	---	2.775	0.91788	0.25	0.35119	0.35	1.90526	0.525	1.41038	0.175	0.05	0.675	1.17131	0.125	0.88081	0.65	1.02794
1625831_at	---	---	2.65	2.08886	1.925	2.13756	0.85	2.62996	-0.25	1.79722	0.2	0.18257	0.675	0.35	0.05	0.26458	0.05	0.35119
1631349_a_at	---	---	2.55	0.20817	1.325	0.12583	-0.575	1.06888	0.425	1.35739	-0.85	0.20817	0.6	0.29439	-0.325	0.12583	-0.2	0.29439
1633795_a_at	CG17124	CG17124	2.575	0.97082	1.25	1.62583	-0.7	1.15181	0.1	1.71659	-1.3	0.92014	0.6	1.74547	-1.275	0.263	1.25	1.10310
1634266_at	---	---	2.725	0.3304	0.825	1.42916	-1.025	1.07078	-0.1	1.1225	-1.325	1.29968	0.6	0.36515	-0.9	0.8224	-1.225	1.46373
1637046_at	l(2)03659	Hsp related	2.725	0.70887	0.9	1.00995	0.725	1.84459	-0.175	1.85719	0.075	0.75	0.525	0.43493	-0.325	0.78899	0.55	0.35119
1630505_a_at	Cyp311a1	Cyp311a1	2.775	1.49972	1.225	2.30705	1.625	0.92511	1.05	2.12368	0.825	0.6994	0.525	0.35	0.35	0.6245	0.075	0.38622
1633768_at	CG31814	CG31814	2.375	0.263	0.75	0.1291	0.4	0.11547	0.75	0.27538	0.825	0.19149	0.475	0.27538	-0.125	0.28723	0.275	0.263
1637962_at	spire	spire	2.725	1.35984	1.575	1.61323	0.275	1.40089	0.025	1.10868	-0.125	0.1893	0.45	0.05774	-0.15	0.05774	-0.225	0.20616
1623736_at	tth	trachealless	2.6	0.8756	0.9	1.77951	-0.425	1.65605	0.45	0.51962	0.425	0.1893	0.45	0.52599	0.4	0.36515	-0.05	0.41231
1637666_at	CG15651	CG15651	2.925	0.68496	0.2	0.29439	-0.625	0.78475	0.375	0.57373	0.45	0.34157	0.45	0.28868	-0.075	0.45	-0.3	0.34641
1640600_at	CG34286	CG34286	2.55	0.63509	1.05	0.6455	0.85	0.31091	0.4	0.14142	0.675	0.09574	0.425	0.95171	-2.15	0.52939	1.475	1.04043
1627513_at	---	---	2.85	0.79373	0.975	0.87321	1.925	1.74428	0.825	0.83016	0.875	1.34505	0.375	1.29196	0.65	2.7332	-0.25	0.70887
1624716_at	---	---	2.85	0.41231	1.8	0.45641	0.4	0.29439	0.275	0.17078	-0.225	0.05	0.35	0.1291	-0.225	0.09574	0.025	0.23629
1639106_at	Grip	Glutamate receptor binding protein	3.15	0.65574	1.8	2.02155	1.825	1.73469	0.125	1.59661	-1.575	1.55215	0.225	0.38622	0.025	0.1893	0.125	0.20616
1625628_at	---	---	2.4	0.31623	0.4	0.14142	-0.25	2.04206	-0.425	0.63966	0.05	0.1291	0.2	0.23094	-0.025	0.12583	0.1	0.23094
1635372_a_at	Mf	Zeel1	2.825	1.39613	0.6	0.58878	1.025	0.53151	0.75	0.67577	-1.25	2.25758	-0.175	0.78899	0.025	2.39357	-0.725	0.17078
1631501_at	CG41057	CG41057	2.825	0.86023	1.125	0.91424	1.625	1.48633	0.8	0.43205	0.25	0.20817	0.15	0.31091	-0.225	0.22174	-0.525	0.32016
1629928_a_at	CG32141	CG32141	2.7	0.41633	0.025	0.29861	0.075	1.48633	1.35	1.56098	0.025	0.27538	0.1	0.27538	-0.1	0.29439	-0.35	0.25166
1635963_a_at	CG7990	CG7990	2.625	0.05	2.15	0.1291	-1.025	1.03078	0.075	0.30957	0.25	0.1291	0.1	0.11547	0.15	0.1291	0.075	0.15
163189_at	Drs	Drosomycin	2.7	1.17473	1.525	2.00728	-0.475	1.05633	0.15	1.34288	-0.15	1.96044	0.1	0.3266	-0.8	1.48773	-1.4	1.42829
1640311_at	---	---	2.675	0.61305	-0.4	0.60553	-0.075	0.78899	-0.275	0.68981	0.3	0.21602	0.05	0.19149	-0.025	0.20616	-0.4	0.18257
1624287_at	CG17217	CG17217	2.45	0.47958	1.75	2.16256	1.3	0.38297	0.7	0.33665	0.075	0.263	0.05	0.53229	-0.025	0.05	0.025	0.34034
1624590_at	CG17134	CG17134	2.775	0.73655	2.05	1.49332	-0.35	0.91469	0.425	0.32016	-0.1	0.1633	0.05	0.23805	-0.2	0.18257	-0.275	0.263
1635031_s_at	CG11147	CG11147	2.35	0.19149	1.35	1.22338	0.9	0.40825	0.85	0.31091	0.6	0.1633	0.05	0.23805	-0.175	0.15	-0.275	0.22174
1636743_s_at	---	---	2.625	1.02429	1.95	1.09087	0.7	0.45461	0.375	0.3594	0.125	0.17078	0.025	0.05	0.40731	-0.325	0.22174	
1640848_at	CG11597	PP4-like	2.975	0.37749	1.975	1.42916	0.825	0.32016	1.25	1.33041	0.825	0.59652	-0.025	1.60286	0.25	0.81854	-0.225	1.25
1631233_at	Hh3	CG10296	2.35	1.13871	-0.1	0.08165	-0.25	0.46347	-0.525	0.69462	0.125	0.09574	-0.025	0.32016	-0.425	0.09574	-0.6	0.29439
1636571_at	Rtn12	tropomyosin-like	2.35	0.05774	0.975	1.07819	2.1	1.82392	1.9	1.52096	0.05	0.70475	-0.05	0.1291	-0.475	0.27538	-0.675	0.05
1623397_at	---	---	2.325	0.86168	1.95	1.80093	-0.825	1.60909	1.15	1.40594	0.05	0.1291	-0.05	0.20817	-0.3	0.21602	-0.35	0.1291
1625986_at	Ku80	CG31826,Ku80	2.325	0.89582	1.625	0.9535	0.425	2.13912	-0.775	1.4523	-0.175	0.4717	-0.075	0.22174	-0.5	0.24495	0.65	0.23805
163720_at	CG4440	CG4440	2.425	0.263	1.65	1.96723	2.3	0.21602	1	1.00333	0.2	0.36515	-0.075	0.20616	-0.5	0.2582	-0.35	0.1291
1630522_a_at	ST6Gal	siatransferase-like	2.825	0.62383	2.225	0.51235	0.95	0.3	0.525	0.1893	-0.325	0.17078	-0.2	0.18257	-0.425	0.09574	-0.075	0.36856
1627164_at	CG4616	CG4616	3.6	0.69761	0.3	0.2708	1.575	0.74106	1.425	0.98784	0.025	0.09574	-0.25	0.36968	-0.35	0.36968	-0.575	0.12583
1623791_s_at	Rab9D,Rab9Db,Rab9E,Rab9F	Rab9D,CG9807,CG32673,CG32671	2.825	0.22174	1.7	0.90185	0.625	0.12583	2.05	0.16348	-0.075	0.20616	-0.4	0.45461	-0.275	0.22174	0.025	0.40311
1637721_at	CG3301	CG3301	2.8	0.98658	0.15	0.23805	-0.05	0.87369	0.375	0.9215	-0.15	0.41231	-0.425	0.22174	-0.85	0.33166	-0.775	0.28723
1631066_at	rib	ribbon	2.55	0.83467	0.2	0.2708	0.85	0.75939	0.95	1.18181	0.4	0.23094	-0.45	0.20817	-0.55	0.05774	-0.75	0.23805
1640473_at	CG34120	CG34120	2.35	0.65574	1.6	0.8756	0.225	1.22848	0.15	3.0256	0.975	1.22848	-0.55	0.26458	0.875	0.74106	-0.525	0.28723
1641555_at	CG32169	CG32169	2.6	1.3412	0.9	1.30884	-0.15	0.71414	-1.675	0.29861	-1.275	1.63376	-0.575	0.97425	-0.45			